

Chao-Dong Zhu

List of Publications by Year in descending order

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157
papers

3,953
citations

126907

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163
all docs

163
docs citations

163
times ranked

5297
citing authors

#	ARTICLE	IF	CITATIONS
1	Impacts of species richness on productivity in a large-scale subtropical forest experiment. <i>Science</i> , 2018, 362, 80-83.	12.6	433
2	Comparison of Methods for Molecular Species Delimitation Across a Range of Speciation Scenarios. <i>Systematic Biology</i> , 2018, 67, 830-846.	5.6	277
3	Sampling biases shape our view of the natural world. <i>Ecography</i> , 2021, 44, 1259-1269.	4.5	190
4	Biodiversity across trophic levels drives multifunctionality in highly diverse forests. <i>Nature Communications</i> , 2018, 9, 2989.	12.8	169
5	Global Patterns and Drivers of Bee Distribution. <i>Current Biology</i> , 2021, 31, 451-458.e4.	3.9	155
6	Performance of criteria for selecting evolutionary models in phylogenetics: a comprehensive study based on simulated datasets. <i>BMC Evolutionary Biology</i> , 2010, 10, 242.	3.2	141
7	Working landscapes need at least 20% native habitat. <i>Conservation Letters</i> , 2021, 14, e12773.	5.7	116
8	Hepatitis B virus subgenotyping: History, effects of recombination, misclassifications, and corrections. <i>Infection, Genetics and Evolution</i> , 2013, 16, 355-361.	2.3	89
9	Potential efficacy of mitochondrial genes for animal DNA barcoding: a case study using eutherian mammals. <i>BMC Genomics</i> , 2011, 12, 84.	2.8	83
10	The complete mitochondrial genome of the yellow coaster, <i>Acraea aëssa</i> (Lepidoptera: Nymphalidae). <i>Molecular Biology Reports</i> , 2010, 37, 3431-3438.	2.3	79
11	A fuzzy set theory based approach to analyse species membership in DNA barcoding. <i>Molecular Ecology</i> , 2012, 21, 1848-1863.	3.9	73
12	Estimating sample sizes for DNA barcoding. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 1035-1039.	2.7	70
13	Characterization of the Complete Mitochondrion Genome of Diurnal Moth <i>Amata emma</i> (Butler) (Lepidoptera: Erebidæ) and Its Phylogenetic Implications. <i>PLoS ONE</i> , 2013, 8, e72410.	2.5	62
14	Phylogenomics from low coverage whole genome sequencing. <i>Methods in Ecology and Evolution</i> , 2019, 10, 507-517.	5.2	59
15	The Mitochondrial Genome of <i>Elodia flavipalpis</i> Aldrich (Diptera: Tachinidae) and the Evolutionary Timescale of Tachinid Flies. <i>PLoS ONE</i> , 2013, 8, e61814.	2.5	51
16	Genetic analysis of four porcine avian influenza viruses isolated from Shandong, China. <i>Archives of Virology</i> , 2008, 153, 211-217.	2.1	50
17	Late Pleistocene population expansion of <i>Scylla paramamosain</i> along the coast of China: A population dynamic response to the Last Interglacial sea level highstand. <i>Journal of Experimental Marine Biology and Ecology</i> , 2010, 385, 20-28.	1.5	49
18	Global and Local Persistence of Influenza A(H5N1) Virus. <i>Emerging Infectious Diseases</i> , 2014, 20, 1287-1295.	4.3	49

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19	Positive selection on hemagglutinin and neuraminidase genes of H1N1 influenza viruses. <i>Virology Journal</i> , 2011, 8, 183.	3.4	48
20	Phylogenetic Reconstruction and DNA Barcoding for Closely Related Pine Moth Species (<i>Dendrolimus</i>) in China with Multiple Gene Markers. <i>PLoS ONE</i> , 2012, 7, e32544.	2.5	48
21	DNA barcoding of six <i>Ceroplastes</i> species (Hemiptera: Coccoidea: Coccidae) from China. <i>Molecular Ecology Resources</i> , 2012, 12, 791-796.	4.8	47
22	Molecular phylogeny reveals independent origins of body scales in Entomobryidae (Hexapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62.	2.7	47
23	The complete mitochondrial genome of <i>Spilonota lechriaspis</i> Meyrick (Lepidoptera: Tortricidae). <i>Molecular Biology Reports</i> , 2011, 38, 3757-3764.	2.3	46
24	Identification of novel inter-genotypic recombinants of human hepatitis B viruses by large-scale phylogenetic analysis. <i>Virology</i> , 2012, 427, 51-59.	2.4	44
25	Tree phylogenetic diversity promotes host-parasitoid interactions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160275.	2.6	41
26	Toward a methodical framework for comprehensively assessing forest multifunctionality. <i>Ecology and Evolution</i> , 2017, 7, 10652-10674.	1.9	41
27	The complete mitochondrial genome of the cockroach <i>Eupolyphaga sinensis</i> (Blattaria: Polyphagidae) and the phylogenetic relationships within the Dictyoptera. <i>Molecular Biology Reports</i> , 2010, 37, 3509-3516.	2.3	40
28	The complete mitochondrial genome of <i>Choristoneura longicellana</i> (Lepidoptera: Tortricidae) and phylogenetic analysis of Lepidoptera. <i>Gene</i> , 2016, 591, 161-176.	2.2	40
29	The mitochondrial genome of the butterfly <i>Papilio xuthus</i> (Lepidoptera: Papilionidae) and related phylogenetic analyses. <i>Molecular Biology Reports</i> , 2010, 37, 3877-3888.	2.3	39
30	A Simulation-Based Evaluation of Tip-Dating Under the Fossilized Birth-Death Process. <i>Systematic Biology</i> , 2020, 69, 325-344.	5.6	39
31	A Complete Analysis of HA and NA Genes of Influenza A Viruses. <i>PLoS ONE</i> , 2010, 5, e14454.	2.5	38
32	The significance of tree-tree interactions for forest ecosystem functioning. <i>Basic and Applied Ecology</i> , 2021, 55, 33-52.	2.7	38
33	Complete mitochondrial genomes of two cockroaches, <i>Blattella germanica</i> and <i>Periplaneta americana</i> , and the phylogenetic position of termites. <i>Current Genetics</i> , 2012, 58, 65-77.	1.7	36
34	Cryptic diversity, diversification and vicariance in two species complexes of <i>Tomocerus</i> (<i>Tomocerus</i>) (<i>Tomocerus</i>) (<i>Tomoceridae</i>) from China. <i>Zoologica Scripta</i> , 2014, 43, 393-404.	1.7	36
35	Multiple components of plant diversity loss determine herbivore phylogenetic diversity in a subtropical forest experiment. <i>Journal of Ecology</i> , 2019, 107, 2697-2712.	4.0	33
36	The Integrative Taxonomic Approach Reveals Host Specific Species in an Encyrtid Parasitoid Species Complex. <i>PLoS ONE</i> , 2012, 7, e37655.	2.5	32

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37	Complete sequence of the mitochondrial genome of the Japanese buff-tip moth, <i>Phalera flavescens</i> (Lepidoptera: Notodontidae). <i>Genetics and Molecular Research</i> , 2012, 11, 4213-4225.	0.2	30
38	The Complete Mitochondrial Genome of <i>Leucoptera malifoliella</i> Costa (Lepidoptera: Lyonetiidae). <i>DNA and Cell Biology</i> , 2012, 31, 1508-1522.	1.9	28
39	A simulation study of sample size for DNA barcoding. <i>Ecology and Evolution</i> , 2015, 5, 5869-5879.	1.9	28
40	Recombination in Hepatitis C Virus: Identification of Four Novel Naturally Occurring Inter-Subtype Recombinants. <i>PLoS ONE</i> , 2012, 7, e41997.	2.5	27
41	DNA barcoding of endoparasitoid wasps in the genus <i>Anicetus</i> reveals high levels of host specificity (Hymenoptera: Encyrtidae). <i>Biological Control</i> , 2011, 58, 182-191.	3.0	26
42	The complete mitochondrial genome of the endangered Apollo butterfly, <i>Parnassius apollo</i> (Lepidoptera: Papilionidae) and its comparison to other Papilionidae species. <i>Journal of Asia-Pacific Entomology</i> , 2014, 17, 663-671.	0.9	26
43	Three questions: How can taxonomists survive and thrive worldwide?. <i>Megataxa</i> , 2020, 1, .	3.8	26
44	Subgenotyping of Genotype C Hepatitis B Virus: Correcting Misclassifications and Identifying a Novel Subgenotype. <i>PLoS ONE</i> , 2012, 7, e47271.	2.5	26
45	Taxonomy must engage with new technologies and evolve to face future challenges. <i>Nature Ecology and Evolution</i> , 2021, 5, 3-4.	7.8	25
46	Ultraconserved element phylogenomics and biogeography of the agriculturally important mason bee subgenus <i>Osmia</i> (<i>Osmia</i>). <i>Systematic Entomology</i> , 2021, 46, 453-472.	3.9	25
47	Host functional and phylogenetic composition rather than host diversity structure plant herbivore networks. <i>Molecular Ecology</i> , 2020, 29, 2747-2762.	3.9	24
48	A review of the Chinese <i>Diglyphus</i> Walker (Hymenoptera: Eulophidae). <i>Oriental Insects</i> , 2000, 34, 263-288.	0.3	23
49	The Complete Mitochondrial Genome of the Rice Moth, <i>Corcyra cephalonica</i> . <i>Journal of Insect Science</i> , 2012, 12, 1-14.	1.5	23
50	Resolving the phylogeny of a speciose spider group, the family Linyphiidae (Araneae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 135-149.	2.7	23
51	Molecular phylogeny and the underestimated species diversity of the endemic white-bellied rat (Rodentia: Muridae: <i>Niviventer</i>) in Southeast Asia and China. <i>Zoologica Scripta</i> , 2015, 44, 475-494.	1.7	22
52	<i>Diglyphus isaea</i> (Hymenoptera: Eulophidae): a probable complex of cryptic species that forms an important biological control agent of agromyzid leaf miners. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2007, 45, 128-135.	1.4	20
53	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012, 12, 116.	2.0	20
54	Mitochondrial phylogeography of a leafminer parasitoid, <i>Diglyphus isaea</i> (Hymenoptera: Eulophidae) in China. <i>Biological Control</i> , 2006, 38, 380-389.	3.0	19

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55	Molecular signatures of X chromosome inactivation and associations with clinical outcomes in epithelial ovarian cancer. <i>Human Molecular Genetics</i> , 2019, 28, 1331-1342.	2.9	19
56	Scanning electron microscopy studies of antennal sensilla of <i>Ooencyrtus phongi</i> (Hymenoptera: Encyrtidae). <i>Microscopy Research and Technique</i> , 2011, 74, 936-945.	2.2	18
57	New insights into the phylogeny of fig pollinators using Bayesian analyses. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 306-315.	2.7	17
58	Description of <i>Synergus castaneus</i> n. sp. (Hymenoptera: Cynipidae: Synergini) Associated with an Unknown Gall on <i>Castanea</i> spp. (Fagaceae) in China. <i>Annals of the Entomological Society of America</i> , 2013, 106, 437-446.	2.5	17
59	Two new <i>Aprostocetus</i> species (Hymenoptera: Eulophidae: Tetrastichinae), fortuitous parasitoids of invasive eulophid gall inducers (Tetrastichinae) on Eucalyptus and Erythrina. <i>Zootaxa</i> , 2014, 3846, 261-72.	0.5	17
60	Life history and biocontrol potential of the first female-producing parthenogenetic species of <i>Diglyphus</i> (Hymenoptera: Eulophidae) against agromyzid leafminers. <i>Scientific Reports</i> , 2018, 8, 3222.	3.3	16
61	Small Mammal Investigation in Spotted Fever Focus with DNA-Barcoding and Taxonomic Implications on Rodents Species from Hainan of China. <i>PLoS ONE</i> , 2012, 7, e43479.	2.5	16
62	Ovipositor length of three Apocrypta species: Effect on oviposition behavior and correlation with syconial thickness. <i>Phytoparasitica</i> , 2005, 33, 113-120.	1.2	15
63	Quantifying Species Diversity with a DNA Barcoding-Based Method: Tibetan Moth Species (Noctuidae) on the Qinghai-Tibetan Plateau. <i>PLoS ONE</i> , 2013, 8, e64428.	2.5	15
64	A Unique Nest-Protection Strategy in a New Species of Spider Wasp. <i>PLoS ONE</i> , 2014, 9, e101592.	2.5	15
65	A DNA Barcoding system integrating multigene sequence data. <i>Methods in Ecology and Evolution</i> , 2015, 6, 930-937.	5.2	15
66	Construction, implementation and testing of an image identification system using computer vision methods for fruit flies with economic importance (Diptera: Tephritidae). <i>Pest Management Science</i> , 2017, 73, 1511-1528.	3.4	14
67	Application of DNA barcoding to the identification of Hymenoptera parasitoids from the soybean aphid (<i>Aphis glycines</i>) in China. <i>Insect Science</i> , 2014, 21, 363-373.	3.0	13
68	Formal nomenclature and description of cryptic species of the <i>Encyrtus sasakii</i> complex (Hymenoptera: Encyrtidae). <i>Scientific Reports</i> , 2016, 6, 34372.	3.3	13
69	A High-quality Draft Genome Assembly of <i>Sinella curviseta</i> : A Soil Model Organism (Collembola). <i>Genome Biology and Evolution</i> , 2019, 11, 521-530.	2.5	13
70	The complete mitochondrial genome of the <i>Colletes gigas</i> (Hymenoptera: Colletidae). <i>Open Access Journal of Science</i> , 2017, 10, 142-147.	0.7	12
71	Chinese species of <i>Pediobius</i> Walker (Hymenoptera: Eulophidae). <i>Zootaxa</i> , 2017, 4240, 1-71.	0.5	12
72	The First Draft Genome of the Plasterer Bee <i>Colletes gigas</i> (Hymenoptera: Colletidae: Colletes). <i>Genome Biology and Evolution</i> , 2020, 12, 860-866.	2.5	12

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73	Multi-trophic communities re-establish with canopy cover and microclimate in a subtropical forest biodiversity experiment. <i>Oecologia</i> , 2021, 196, 289-301.	2.0	12
74	Phylogeography of the mud crab (<i>Scylla serrata</i>) in the Indo-West Pacific reappraised from mitochondrial molecular and oceanographic clues: transoceanic dispersal and coastal sequential colonization. <i>Marine Ecology</i> , 2011, 32, 52-64.	1.1	11
75	A review of the Colletes succinctus-group (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF Zootaxa, 2013, 3626, 173-187.	0.5	11
76	Investigating the Parasitoid Community Associated with the Invasive Mealybug Phenacoccus solenopsis in Southern China. <i>Insects</i> , 2021, 12, 290.	2.2	11
77	Host specificity of parasitoids (Encyrtidae) toward armored scale insects (Diaspididae): Untangling the effect of cryptic species on quantitative food webs. <i>Ecology and Evolution</i> , 2018, 8, 7879-7893.	1.9	10
78	Intra- and interspecific tree diversity promotes multitrophic plant-Hemiptera ant interactions in a forest diversity experiment. <i>Basic and Applied Ecology</i> , 2018, 29, 89-97.	2.7	9
79	<p>Bees of the Colletes clypearis-group (Hymenoptera: Apoidea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	0.5	8
80	A Protocol for Species Delineation of Public DNA Databases, Applied to the Insecta. <i>Systematic Biology</i> , 2014, 63, 712-725.	5.6	8
81	Sequencing and characterization of the <i>Megachile sculpturalis</i> (Hymenoptera: Megachilidae) mitochondrial genome. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 344-346.	0.7	8
82	New records of bees of the genus <i>Sphecodes</i> Latreille in the Palaearctic part of China (Hymenoptera, Tj ETQq0 0 0.19 rgBT /Overlock 10 TF	1.9	8
83	Tree diversity promotes predatory wasps and parasitoids but not pollinator bees in a subtropical experimental forest. <i>Basic and Applied Ecology</i> , 2021, 53, 134-142.	2.7	8
84	Phylogenetic relatedness, functional traits, and spatial scale determine herbivore co-occurrence in a subtropical forest. <i>Ecological Monographs</i> , 2022, 92, e01492.	5.4	8
85	Bees of the Colletes flavicornis-group from China with description of one new species (Hymenoptera: Apoidea: Colletidae). <i>Zootaxa</i> , 2014, 3780, 534.	0.5	7
86	The Bees of the Genus <i>Colletes</i> (Hymenoptera: Apoidea: Colletidae) from China. <i>Zootaxa</i> , 2014, 3856, 451-83.	0.5	7
87	The complete mitochondrial genome of <i>Carposina sasakii</i> (Lepidoptera: Carposinidae). <i>Mitochondrial DNA</i> , 2016, 27, 1432-1434.	0.6	7
88	Parasitoid-host associations of the genus <i>Coccophagus</i> (Hymenoptera: Aphelinidae) in China. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 38-49.	2.3	7
89	Testing the systematic status of <i>Homalictus</i> and <i>Rostrohalictus</i> with weakened cross-vein groups within Halictini (Hymenoptera: Halictidae) using low-coverage whole-genome sequencing. <i>Insect Science</i> , 2022, 29, 1819-1833.	3.0	7
90	The variable codons of H5N1 avian influenza A virus haemagglutinin genes. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 987-993.	1.3	6

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91	Positive selection analysis of VP1 Genes of worldwide human enterovirus 71 viruses. <i>Virologica Sinica</i> , 2009, 24, 59-64.	3.0	6
92	Preliminary phylogeny of the genus <i>Copidosoma</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td (<scp>H</scp>ymenoptera,) 2014, 39, 325-334.	3.9	6
93	Sequencing and characterization of the <i>Megachile strupigera</i> (Hymenoptera: Megachilidae) mitochondrial genome. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 282-284.	0.4	6
94	Revision of the <i>Anthidiellum</i> Cockerell, 1904 of China (Hymenoptera, Apoidea,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td (<scp>H</scp>ymenoptera,) 2014, 39, 325-334.	0.5	6
95	Comparison of the pollination efficiency of <i>Apis cerana</i> with wild bees in oil-seed camellia fields. <i>Basic and Applied Ecology</i> , 2021, 56, 250-258.	2.7	6
96	A new species of <i>Oomyzus Rondani</i> (Hymenoptera, Eulophidae) reared from the pupae of <i>Coccinella septempunctata</i> (Coleoptera, Coccinellidae) in China. <i>ZooKeys</i> , 2020, 953, 49-60.	1.1	6
97	Morphological and molecular identification of arrhenotokous strain of <i>Diglyphus wani</i> (Hymenoptera, Eulophidae) found in China as a control agent against agromyzid leafminers. <i>ZooKeys</i> , 2021, 1071, 109-126.	1.1	6
98	A study of <i>Platyplectrus Ferrière</i> (Hymenoptera: Eulophidae) in mainland China. <i>Journal of Natural History</i> , 2004, 38, 2183-2209.	0.5	5
99	A new species of <i>Bathanthidium Mavromoustakis</i> (Hymenoptera: Megachilidae: Anthidiini) from China, with a key to the species. <i>Zootaxa</i> , 2012, 3218, 59.	0.5	5
100	The complete mitochondrial genome of <i>Acleris fimbriana</i> (Lepidoptera: Tortricidae). <i>Mitochondrial DNA</i> , 2016, 27, 1-3.	0.6	5
101	gPGA: GPU Accelerated Population Genetics Analyses. <i>PLoS ONE</i> , 2015, 10, e0135028.	2.5	5
102	Selection pressure on Haemagglutinin genes of H9N2 influenza viruses from different hosts. <i>Virologica Sinica</i> , 2009, 24, 65-70.	3.0	4
103	A review of the genus <i>Monema</i> Walker in China (Lepidoptera, Limacodidae). <i>ZooKeys</i> , 2013, 306, 23-36.	1.1	4
104	A systematic study of <i>Ichneumonosoma de Meijere</i> , <i>Pelmatops Enderlein</i> , <i>Pseudopelmatops Shiraki</i> and <i>Soita Walker</i> (Diptera: Tephritidae). <i>Zootaxa</i> , 2015, 4013, 301-47.	0.5	4
105	Descriptions of three new species of <i>Dzhanokmenia</i> (Hymenoptera: Eulophidae) from China. <i>Zootaxa</i> , 2016, 4121, 447.	0.5	4
106	Relationships between wild bee abundance and fruit set of <i>Camellia oleifera</i> Abel. <i>Journal of Applied Entomology</i> , 2021, 145, 277-285.	1.8	4
107	Foraging Behavior of Honeybees (<i>Apis Mellifera</i> L.) and Ground Bumblebees (<i>Bombus Terrestris</i> L.) and its Influence on Seed Yield and Oil Quality of Oil Tree Peony Cultivar "Fengdan" (Paeonia Ostii T. Hong) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td (<scp>H</scp>ymenoptera,) 2014, 39, 325-334.	0.4	4
108	Revision of Chinese <i>Euplectromorpha Girault</i> (Hymenoptera: Eulophidae). <i>Insect Systematics and Evolution</i> , 2000, 31, 401-410.	0.7	3

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109	First record of the bee genus <i>Homalictus</i> Cockerell for China with description of a new species (Hymenoptera: Apoidea: Megachilidae). <i>Zootaxa</i> , 2017, 4317, 391.	1.4	3
110	Observational natural history and morphological taxonomy are indispensable for future challenges in biodiversity and conservation. <i>Communicative and Integrative Biology</i> , 2015, 8, e992745.	0.5	3
111	Notes on <i>Kocourekia boučeki</i> (Hymenoptera: Eulophidae: Tetrastichinae) with description of a new species from China. <i>Zootaxa</i> , 2017, 4317, 391.	0.5	3
112	Revision of the bee genus <i>Bathanthidium</i> Mavromoustakis (Hymenoptera: Apoidea: Megachilidae). <i>Zootaxa</i> , 2017, 4317, 391.	0.5	3
113	A review of stalk-eyed fruit flies (Diptera: Tephritidae: Trypetinae). <i>Zootaxa</i> , 2010, 2654, 1.	0.5	3
114	Integrative taxonomy based on morphometric and molecular data supports recognition of the three cryptic species within the <i>Encyrtus sasakii</i> complex (Hymenoptera, Encyrtidae). <i>Journal of Hymenoptera Research</i> , 0, 90, 129-152.	0.8	3
115	Genetic imprints of paleo-oceanographic conditions in the Chinese seas: Population bottlenecks of <i>Scylla paramamosain</i> and <i>Periophthalmus modestus</i> inferred from mitochondrial genes. <i>Journal of Earth Science (Wuhan, China)</i> , 2010, 21, 237-240.	3.2	2
116	<i>Astymachus</i> and <i>Boucekiella</i> (Hymenoptera: Encyrtidae) from China. <i>Oriental Insects</i> , 2010, 44, 11-16.	0.3	2
117	Heuristic optimization for global species clustering of DNA sequence data from multiple loci. <i>Methods in Ecology and Evolution</i> , 2013, 4, 961-970.	5.2	2
118	New species and records of Trypetinae (Diptera: Tephritidae) from China. <i>Zootaxa</i> , 2013, 3710, 333.	0.5	2
119	A new phytophagous eulophid wasp (Hymenoptera: Chalcidoidea: Eulophidae) that feeds within leaf buds and cones of <i>Pinus massoniana</i> . <i>Zootaxa</i> , 2014, 3753, 391.	0.5	2
120	A review of the genus <i>Triancyra</i> Baltazar (Ichneumonidae: Rhyssinae) from Vietnam, with descriptions of three new species. <i>Zootaxa</i> , 2018, 4377, 565.	0.5	2
121	The mitochondrial genome of <i>Platencyrtus parkeri</i> Feriere (Hymenoptera: Encyrtidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3479-3481.	0.4	2
122	Chinese species of <i>Nomia</i> (<i>Gnathonomia</i>) Pauly, 2005 (Hymenoptera: Apoidea: Megachilidae). <i>Zootaxa</i> , 2017, 4317, 391.	0.5	2
123	Nesting and foraging behavior of <i>Xylocopa valga</i> in the Ejina Oasis, China. <i>PLoS ONE</i> , 2020, 15, e0235769.	2.5	2
124	Phylogeny of Adramini (Diptera, Tephritidae) based on integrative evidence. <i>Zoologica Scripta</i> , 2021, 50, 71-83.	1.7	2
125	Comparison of two criteria on the essential number calculation of <i>Andrena camellia</i> . <i>Bulletin of Entomological Research</i> , 2021, 111, 364-370.	1.0	2
126	A newly recorded Subgenus <i>Sudila</i> from China with description of two new species (Hymenoptera: Apoidea: Megachilidae). <i>Zootaxa</i> , 2017, 4317, 391.	0.5	2

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127	Parallel Metropolis Coupled Markov Chain Monte Carlo for Isolation with Migration Model. <i>Applied Mathematics and Information Sciences</i> , 2013, 7, 219-224.	0.5	2
128	The First Biological Portrait of Stalk-Eyed Fruit Flies: Life History, Reproductive Biology and Host Use Patterns in <i>Pelmatops</i> spp. (Diptera: Tephritidae). <i>Annals of the Entomological Society of America</i> , 2022, 115, 365-377.	2.5	2
129	A new species of <i>Zagrammosoma</i> Ashmead (Hymenoptera, Eulophidae) from Qinghai Province, China. <i>ZooKeys</i> , 2014, 417, 45-55.	1.1	1
130	Genetic Variability of <i>Melipona subnitida</i> (Hymenoptera: Apidae) in Introduced and Native Populations. <i>Journal of Insect Science</i> , 2018, 18, .	1.5	1
131	Nesting Biology of <i>Xylocopa xinjiangensis</i> (Hymenoptera: Apidae: Xylocopinae). <i>Journal of Insect Science</i> , 2018, 18, .	1.5	1
132	A taxonomic study of Chinese species of <i>Copidosomopsis</i> Girault (Hymenoptera: Encyrtidae). <i>Zootaxa</i> , 2010, 2490, .	0.5	1
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150	China: Change tack to boost basic research. <i>Nature</i> , 2016, 536, 30-30.	27.8	0
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156	Global invasion risk of <i>Apocephalus borealis</i> , a honey bee parasitoid. <i>Apidologie</i> , 2021, 52, 1128-1140.	2.0	0
157	Key to <i>Ooctonus</i> Haliday (Hymenoptera: Mymaridae) in China, with one new species and three new country records. <i>Zootaxa</i> , 2022, 5155, 581-588.	0.5	0